

SEQUENCE LISTING



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(1) GENERAL INFORMATION:

- (i) APPLICANT: Botella, Jose Ramon
- (ii) TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
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 - (C) CITY: Princeton
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 08540-3662
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/043,627
 - (B) FILING DATE: 20-MAR-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/AU96/00591
 - (B) FILING DATE: 20-SEP-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU PN5559
 - (B) FILING DATE: 20-SEP-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU PN9603
 - (B) FILING DATE: 02-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Bernstein, Scott N.
 - (B) REGISTRATION NUMBER: 38,827
 - (C) REFERENCE/DOCKET NUMBER: 3573-11US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 609-924-8555
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1080 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG	ATG	GGG	TTT	GCG	GAG	AAC	CAG	CTT	TCG	CTG	GAG	TTA	ATA	CGT	GAG	48
Gln	Met	Gly	Phe	Ala	Glu	Asn	Gln	Leu	Ser	Leu	Glu	Leu	Ile	Arg	Glu	
1				5				10						15		
TGG	ATC	AAG	AAT	CAC	CCG	GAG	GCC	TCC	ATT	TGC	TCG	GCG	GAG	GGC	CTG	96
Trp	Ile	Lys	Asn	His	Pro	Glu	Ala	Ser	Ile	Cys	Ser	Ala	Glu	Gly	Leu	
			20					25					30			
CCG	CAG	TTC	ATG	GAG	ATC	GCC	AAT	TTC	CAA	GAC	TAC	CAT	GGC	TTG	CCG	144
Pro	Gln	Phe	Met	Glu	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	Pro	
		35					40					45				
GCT	TTT	CTG	CAG	GGA	ATC	GCG	AAA	TTG	ATG	GAG	AAA	GTG	AGA	GGA	GGA	192
Ala	Phe	Leu	Gln	Gly	Ile	Ala	Lys	Leu	Met	Glu	Lys	Val	Arg	Gly	Gly	
	50					55					60					
AGG	GTC	AAA	TTC	GAT	CCG	AAC	CGC	GTG	GTG	ATG	AGC	GGC	GGA	GGC	ACT	240
Arg	Val	Lys	Phe	Asp	Pro	Asn	Arg	Val	Val	Met	Ser	Gly	Gly	Gly	Thr	
	65				70					75					80	
GGA	GCG	CAA	GAA	ACG	CTC	GCG	TTT	TGT	CTC	GCT	GAC	CCT	GGC	GAC	GCC	288
Gly	Ala	Gln	Glu	Thr	Leu	Ala	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala	
				85				90						95		
TTC	CTC	GTC	CCA	ACT	CCG	TAC	TAT	CCA	GCA	TTT	AAT	CGC	GAT	CTC	CGG	336
Phe	Leu	Val	Pro	Thr	Pro	Tyr	Tyr	Pro	Ala	Phe	Asn	Arg	Asp	Leu	Arg	
			100					105					110			
TGG	AGA	ACG	GGC	GTC	GAG	CTC	CTC	CCG	GTT	CAC	TGC	AAG	AGC	TCT	AAT	384
Trp	Arg	Thr	Gly	Val	Glu	Leu	Leu	Pro	Val	His	Cys	Lys	Ser	Ser	Asn	
		115					120					125				
CAC	TTC	AGA	GTC	ACC	AAA	ACG	GCG	CTA	GAA	TCG	GCA	TAC	GAG	AAG	GCG	432
His	Phe	Arg	Val	Thr	Lys	Thr	Ala	Leu	Glu	Ser	Ala	Tyr	Glu	Lys	Ala	
	130					135					140					
CGA	AAG	GAT	AAC	ATC	AGA	GTA	AAA	GGA	GTA	CTG	ATA	ACC	AAC	CCA	TCC	480
Arg	Lys	Asp	Asn	Ile	Arg	Val	Lys	Gly	Val	Leu	Ile	Thr	Asn	Pro	Ser	
	145				150					155					160	
AAC	CCG	CTC	GGC	ACG	ACC	ATG	GAT	AAA	CAC	ACG	CTA	CAG	ACC	CTC	GTG	528
Asn	Pro	Leu	Gly	Thr	Thr	Met	Asp	Lys	His	Thr	Leu	Gln	Thr	Leu	Val	
				165				170						175		
AAA	TTC	GTA	AAC	GAA	AGG	AGA	ATC	CAC	CTA	GTC	TGC	GAC	GAG	TTA	TAC	576
Lys	Phe	Val	Asn	Glu	Arg	Arg	Ile	His	Leu	Val	Cys	Asp	Glu	Leu	Tyr	
			180				185						190			
GGC	GCA	ACC	ATC	TTT	AGG	GAG	CCC	AGG	TTC	GTC	AGC	ATC	TCC	GAG	GTA	624
Gly	Ala	Thr	Ile	Phe	Arg	Glu	Pro	Arg	Phe	Val	Ser	Ile	Ser	Glu	Val	
		195					200					205				

ATA GAA GAG GAC CCG AAC TGC GAC AAG AAT CTG ATC CAC ATT GCG TAC	672
Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr	
210 215 220	
AGT CTC TCA AAG GAC TTC GGT CTC CCC GGA TTC CGA GTC GGG ATC GTG	720
Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val	
225 230 235 240	
TAT TCC TAC AAC GAC ACG GTG GTT AGT TGC GCA CGC AGA ATG TCG AGC	768
Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser	
245 250 255	
TTC GGC CTC GTC TCG TCG CAG ACA CAG TAC CTA CTG GCC GCC ATG CTA	816
Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu	
260 265 270	
TCC GGC GAA GAA TTT TTG CCA ACA TTA CTG ACT GAA AGC GCG AAG AGT	864
Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser	
275 280 285	
CTG TCG GAG AGC CAC AGG ATC TTC TCT TCC GGC CTT GAG GAA GTC GAC	912
Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp	
290 295 300	
ATC CGC TGC TTG GAC GGC AAT GCC GGG GTC TTC TGC TGG ATG GAC CTA	960
Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu	
305 310 315 320	
CGG CAC CTC CTC AAA GAA GCC ACC GAA GAC GGC GAG CTC GAG CTG TGG	1008
Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp	
325 330 335	
CGC GTG ATA GTG AAC AAT GTC AAG CTC AAT GTG TCC CCC GGT TCG TCG	1056
Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser	
340 345 350	
TTT TAT TGC GCC GAG CCA GGT TGG	1080
Phe Tyr Cys Ala Glu Pro Gly Trp	
355 360	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu	
1 5 10 15	
Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu	
20 25 30	
Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	

Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly
 50 55 60
 Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Gly Thr
 65 70 75 80
 Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95
 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg
 100 105 110
 Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn
 115 120 125
 His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala
 130 135 140
 Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser
 145 150 155 160
 Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val
 165 170 175
 Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr
 180 185 190
 Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val
 195 200 205
 Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr
 210 215 220
 Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val
 225 230 235 240
 Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser
 245 250 255
 Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu
 260 265 270
 Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
 275 280 285
 Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
 290 295 300
 Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
 305 310 315 320
 Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
 325 330 335
 Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
 340 345 350
 Phe Tyr Cys Ala Glu Pro Gly Trp
 355 360

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAG ATG GGC CTT GCT GAG AAT CAG CTT TGC TTT AAT TTA ATT CAC GAG	48
Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu	
1 5 10 15	
TGG CCG CTG AAA AAC CCA GAA GCC TCC ATT TGT ACA ACA CAA GGA GCA	96
Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala	
20 25 30	
GCT GAA TTC AGA GAT ATA GCT ATC TTT CAA GAT TAT CAT GGC TTG GCT	144
Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala	
35 40 45	
GAA TTC AGA GAG GCT GTT GCA AAG TTT ATG GGG AAA GTG AGA AGA AAC	192
Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn	
50 55 60	
AGA GCT TCA TTT GAC CCT GAT CGG ATT GTT ATG AGT GGA GGA GCA ACT	240
Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr	
65 70 75 80	
GGA GCT CAT GAA ATG ATT GGT TTC TGT TTG GCT GAT CCT GGC GAT GCA	288
Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala	
85 90 95	
TTC TTG GTT CCA ACT CCT TAT TAT CCA GGG TTT GAT AGA GAT TTG AGA	336
Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg	
100 105 110	
TGG AGA ACG GGA GTC AAA CTC ATT CCA GTT GTC TGT GAA AGC TCA AAC	384
Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn	
115 120 125	
GAT TAC CAG ATC ACC ATA GAA GCC CTG GAA GCT GCT TAT GAA ACC GCA	432
Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Tyr Glu Thr Ala	
130 135 140	
CAA GAA GCT GAC ATC AAG GTA AAG GGT TTG GTC ATA ACC AAC CCA TCA	480
Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser	
145 150 155 160	
AAC CCA CTG GGA ACA ATT ATT ACC AAG GAC ACA TTA GAA GCT CTA GTC	528
Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val	
165 170 175	

ACC TTC ACC AAC CAC AAG AAC ATT CAT CTG GTG TGT GAT GAG ATA TAT	576
Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr	
180 185 190	
GCT GGT TAC CGT CTT CAG CCC AGG GCC GAA TTC ACC AGC ATA GCC GAG	624
Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu	
195 200 205	
ATA ATT GAA GAA GAT AAA ATT TGT TGC AAT CGT GAT CTC ATC CAC ATC	672
Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile	
210 215 220	
ATT TAC AGT TTA TCC AAA GAC ATG GGA TTC CCT GGA TTT AGA GTT GGC	720
Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly	
225 230 235 240	
ATT GTG TAT TCA TAC AAT GAT GCA GTG GTG AGT TGT GCT CGT AAG ATG	768
Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met	
245 250 255	
TCG AGC TTC GGC CTA GTA TCT TCG CAA ACC CAG TAT CTG ATT GCA TCC	816
Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser	
260 265 270	
ATG TTA GCA GAC GAT GAA TTT GTA GAC AAA TTT ATT GTA GAG AGC AGA	864
Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg	
275 280 285	
AAG AGG CTG GCA ATG AGA CAT AGT TTT TTC ACA CAA AGA CTT GCT CAA	912
Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln	
290 295 300	
GTA GGC ATT AAC TGT TTA AAA AGC AAT GCT GGT CTT TTT GTG TGG ATG	960
Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met	
305 310 315 320	
GAT TTG CGT AGA CTG CTG AAA GAA CAG ACA TTT GAA GCA GAA ATG GTG	1008
Asp Leu Arg Arg Leu Leu Lys Glu Gln Thr Phe Glu Ala Glu Met Val	
325 330 335	
TTA TGG AGA GTA ATT ATA AAC GAA ATG AAA CTC AAT GTA TCT CCT GGT	1056
Leu Trp Arg Val Ile Ile Asn Glu Met Lys Leu Asn Val Ser Pro Gly	
340 345 350	
TCG TCT TTC CAC TGC TCA GAA CCT GGC TGG TTC AGC GTC TGC TTC GCT	1104
Ser Ser Phe His Cys Ser Glu Pro Gly Trp Phe Ser Val Cys Phe Ala	
355 360 365	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu
 1 5 10 15
 Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala
 20 25 30
 Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala
 35 40 45
 Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn
 50 55 60
 Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr
 65 70 75 80
 Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95
 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg
 100 105 110
 Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn
 115 120 125
 Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Ala Tyr Glu Thr Ala
 130 135 140
 Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser
 145 150 155 160
 Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val
 165 170 175
 Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr
 180 185 190
 Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu
 195 200 205
 Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile
 210 215 220
 Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly
 225 230 235 240
 Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met
 245 250 255
 Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser
 260 265 270
 Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg
 275 280 285
 Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln
 290 295 300
 Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met
 305 310 315 320

Asp Leu Arg Arg Leu Leu Lys Glu Gln Thr Phe Glu Ala Glu Met Val
 325 330 335
 Leu Trp Arg Val Ile Ile Asn Glu Met Lys Leu Asn Val Ser Pro Gly
 340 345 350
 Ser Ser Phe His Cys Ser Glu Pro Gly Trp Phe Ser Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1098 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAG ATG GGT TTT GCT GAA AAT CAG CTT TGC TTT GAT TTG ATC GAG AAG	48
Gln Met Gly Phe Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Lys	
1 5 10 15	
TGG GTT AAA AAG AAT CCC AAT GCT TCC ATC TGC ACA GCT GAA GGG GTT	96
Trp Val Lys Lys Asn Pro Asn Ala Ser Ile Cys Thr Ala Glu Gly Val	
20 25 30	
GAA AAC TTC AAG CAC ATA GCC AAC TTC CAA GAC TAT CAT GGC CTG AAA	144
Glu Asn Phe Lys His Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Lys	
35 40 45	
GAA TTT AGA CAG GAA GTT GCC AAG TTA ATG GGG AAG GCA AGA GGC GGC	192
Glu Phe Arg Gln Glu Val Ala Lys Leu Met Gly Lys Ala Arg Gly Gly	
50 55 60	
AGA GTG ACG TTC GAC CCA GAG CGT ATT GTG ATG AGC GGG GGA GCG ACA	240
Arg Val Thr Phe Asp Pro Glu Arg Ile Val Met Ser Gly Gly Ala Thr	
65 70 75 80	
GGC GCC AGC GAG ACG ATT ATG TTT TGC TTG GCG GAT CCA GGC GAT GCT	288
Gly Ala Ser Glu Thr Ile Met Phe Cys Leu Ala Asp Pro Gly Asp Ala	
85 90 95	
CTT CTG GTT CCC ACT CCT TAC TAT CCT GGA TTC AAT AGG GAC CTG AGA	336
Leu Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asn Arg Asp Leu Arg	
100 105 110	
TGG CGA ACC GGC GTC CAG ATT ATT CCC GTG CAA TGC AGC AGC TCA CAC	384
Trp Arg Thr Gly Val Gln Ile Ile Pro Val Gln Cys Ser Ser Ser His	
115 120 125	

AAT	TTT	ACA	GTA	ACA	CGG	GAA	GCC	GTA	GAG	GCT	GCG	TAC	CAG	AAA	GCT	432
Asn	Phe	Thr	Val	Thr	Arg	Glu	Ala	Val	Glu	Ala	Ala	Tyr	Gln	Lys	Ala	
	130					135					140					
CAA	GAA	GCC	AAC	ATC	AAT	GTC	ACA	GGC	TTG	ATC	ATC	ACC	AAC	CCC	TCG	480
Gln	Glu	Ala	Asn	Ile	Asn	Val	Thr	Gly	Leu	Ile	Ile	Thr	Asn	Pro	Ser	
	145				150				155						160	
AAT	CCG	CTA	GGC	ACC	ACC	TTA	GAC	TCA	CAA	ACA	CTC	CAG	AGC	TTG	GTC	528
Asn	Pro	Leu	Gly	Thr	Thr	Leu	Asp	Ser	Gln	Thr	Leu	Gln	Ser	Leu	Val	
				165					170					175		
ATC	TTC	GTC	AAC	GAC	AAG	ACC	ATC	CAC	CTG	GTC	TGC	GAC	GAA	ATC	TAT	576
Ile	Phe	Val	Asn	Asp	Lys	Thr	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	
			180					185					190			
GCC	GCC	ACC	GTC	TTC	AGC	TCC	CCG	GAG	TTC	GTC	AGC	ATC	GGG	GAG	ATC	624
Ala	Ala	Thr	Val	Phe	Ser	Ser	Pro	Glu	Phe	Val	Ser	Ile	Gly	Glu	Ile	
		195					200					205				
ATC	CAA	GAA	ATG	GAC	GTC	AAC	CGC	GAC	CTT	ATC	CAC	ATC	ATC	TAC	AGC	672
Ile	Gln	Glu	Met	Asp	Val	Asn	Arg	Asp	Leu	Ile	His	Ile	Ile	Tyr	Ser	
	210					215					220					
TTG	TCC	AAA	GAT	ATG	GGT	CTC	CCC	GGT	TTC	CGG	GTA	GGT	ATT	GTG	TAT	720
Leu	Ser	Lys	Asp	Met	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	Tyr	
	225				230					235				240		
TCC	TAC	AAC	GAC	GGT	GTA	TTA	AGC	TGC	GGC	CGG	CGG	ATG	TCG	AGC	TTT	768
Ser	Tyr	Asn	Asp	Gly	Val	Leu	Ser	Cys	Gly	Arg	Arg	Met	Ser	Ser	Phe	
				245					250					255		
GGG	TTG	GTC	TCG	TCA	CAG	ACT	CAA	TAT	TTC	CTG	GCG	ACA	CTG	CTG	TCC	816
Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Ser	
			260					265					270			
GAC	GAC	GAG	TTC	GTC	GAT	TAC	TTC	CTC	CGG	GAA	AGC	TCG	AAG	AGG	CTG	864
Asp	Asp	Glu	Phe	Val	Asp	Tyr	Phe	Leu	Arg	Glu	Ser	Ser	Lys	Arg	Leu	
		275					280					285				
GCG	AGA	AGA	CAC	CAT	AAA	CTC	ACC	AGA	GGG	CTG	GAG	CAA	GTG	GGG	ATA	912
Ala	Arg	Arg	His	His	Lys	Leu	Thr	Arg	Gly	Leu	Glu	Gln	Val	Gly	Ile	
	290					295					300					
AAG	TGC	TTG	AAA	AGC	AAT	GCC	GGA	CTT	TTT	GTG	TGG	ATG	GAC	CTG	CGG	960
Lys	Cys	Leu	Lys	Ser	Asn	Ala	Gly	Leu	Phe	Val	Trp	Met	Asp	Leu	Arg	
	305				310					315					320	
AGG	CTC	CTG	GAA	GGT	CCA	ACG	TCG	TTT	GAT	GCA	GAA	ATG	AAG	CTG	TGG	1008
Arg	Leu	Leu	Glu	Gly	Pro	Thr	Ser	Phe	Asp	Ala	Glu	Met	Lys	Leu	Trp	
				325					330					335		
CGG	ACC	ATC	GTC	AAC	GAC	GTG	AAG	CTG	AAC	GTG	TCG	CCG	GGA	TCT	TCG	1056
Arg	Thr	Ile	Val	Asn	Asp	Val	Lys	Leu	Asn	Val	Ser	Pro	Gly	Ser	Ser	
			340					345					350			
TTC	CAC	GTG	GCG	GAG	CCG	GGG	TGG	TTC	AGA	GTA	TGT	TTC	GCT			1098
Phe	His	Val	Ala	Glu	Pro	Gly	Trp	Phe	Arg	Val	Cys	Phe	Ala			
		355					360					365				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Met Gly Phe Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Lys
 1 5 10 15

Trp Val Lys Lys Asn Pro Asn Ala Ser Ile Cys Thr Ala Glu Gly Val
 20 25 30

Glu Asn Phe Lys His Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Lys
 35 40 45

Glu Phe Arg Gln Glu Val Ala Lys Leu Met Gly Lys Ala Arg Gly Gly
 50 55 60

Arg Val Thr Phe Asp Pro Glu Arg Ile Val Met Ser Gly Gly Ala Thr
 65 70 75 80

Gly Ala Ser Glu Thr Ile Met Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95

Leu Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asn Arg Asp Leu Arg
 100 105 110

Trp Arg Thr Gly Val Gln Ile Ile Pro Val Gln Cys Ser Ser Ser His
 115 120 125

Asn Phe Thr Val Thr Arg Glu Ala Val Glu Ala Ala Tyr Gln Lys Ala
 130 135 140

Gln Glu Ala Asn Ile Asn Val Thr Gly Leu Ile Ile Thr Asn Pro Ser
 145 150 155 160

Asn Pro Leu Gly Thr Thr Leu Asp Ser Gln Thr Leu Gln Ser Leu Val
 165 170 175

Ile Phe Val Asn Asp Lys Thr Ile His Leu Val Cys Asp Glu Ile Tyr
 180 185 190

Ala Ala Thr Val Phe Ser Ser Pro Glu Phe Val Ser Ile Gly Glu Ile
 195 200 205

Ile Gln Glu Met Asp Val Asn Arg Asp Leu Ile His Ile Ile Tyr Ser
 210 215 220

Leu Ser Lys Asp Met Gly Leu Pro Gly Phe Arg Val Gly Ile Val Tyr
 225 230 235 240

Ser Tyr Asn Asp Gly Val Leu Ser Cys Gly Arg Arg Met Ser Ser Phe
 245 250 255

Gly Leu Val Ser Gln Thr Gln Tyr Phe Leu Ala Thr Leu Leu Ser
 260 265 270

Asp Asp Glu Phe Val Asp Tyr Phe Leu Arg Glu Ser Ser Lys Arg Leu
 275 280 285
 Ala Arg Arg His His Lys Leu Thr Arg Gly Leu Glu Gln Val Gly Ile
 290 295 300
 Lys Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg
 305 310 315 320
 Arg Leu Leu Glu Gly Pro Thr Ser Phe Asp Ala Glu Met Lys Leu Trp
 325 330 335
 Arg Thr Ile Val Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser
 340 345 350
 Phe His Val Ala Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAG ATG GGC CTT GCC GAG AAT CAG CTT TGC TTT GAT TTG ATC GAA GAC	48
Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Asp	
1 5 10 15	
TGG ATT CGC AAA AAT CCC TAT GCC TCC ATT TGT ACT GCT GAA GGA GTT	96
Trp Ile Arg Lys Asn Pro Tyr Ala Ser Ile Cys Thr Ala Glu Gly Val	
20 25 30	
GAT GAG TTC AAG GAG ATT GCA AAC TTT CAA GAT TAT CAT GGC TTG CCA	144
Asp Glu Phe Lys Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
GAG TTT AGA AAG GCT GTG GCA AAG TTT ATG GGA AAA GTG AGA GGT GGA	192
Glu Phe Arg Lys Ala Val Ala Lys Phe Met Gly Lys Val Arg Gly Gly	
50 55 60	
AGA GTA ACA TTT GAT CCA GAC CGT ATA GTC ATG GGC GGT GGA GTT ACA	240
Arg Val Thr Phe Asp Pro Asp Arg Ile Val Met Gly Gly Gly Val Thr	
65 70 75 80	
GGC GCA AAC GAG CAA ATC ATC TTC TGT TTA GCC GAC CCT GGC GAT GCT	288
Gly Ala Asn Glu Gln Ile Ile Phe Cys Leu Ala Asp Pro Gly Asp Ala	
85 90 95	

TTT	CTT	GTT	CCC	TCA	CCT	TAT	TAT	CCA	GCA	TTT	GAC	CGG	GAC	CTG	GGA	336
Phe	Leu	Val	Pro	Ser	Pro	Tyr	Tyr	Pro	Ala	Phe	Asp	Arg	Asp	Leu	Gly	
			100					105					110			
TGG	CGC	ACT	GGA	GGT	GAA	ATA	GTT	CCT	GTT	CCC	TGT	GAC	AGC	TCA	ACC	384
Trp	Arg	Thr	Gly	Gly	Glu	Ile	Val	Pro	Val	Pro	Cys	Asp	Ser	Ser	Thr	
			115				120					125				
AAT	TTC	CAG	ATA	ACC	AGA	GAT	GCA	TTG	GAA	GAA	GCA	TAT	GAA	AAA	GCT	432
Asn	Phe	Gln	Ile	Thr	Arg	Asp	Ala	Leu	Glu	Glu	Ala	Tyr	Glu	Lys	Ala	
			130			135					140					
CGA	GAA	GCC	AAC	ATT	AAT	ATT	AAA	GGC	TTG	ATC	ATA	ACA	AAC	CCT	TCA	480
Arg	Glu	Ala	Asn	Ile	Asn	Ile	Lys	Gly	Leu	Ile	Ile	Thr	Asn	Pro	Ser	
145						150					155				160	
AAC	CCA	CTT	GGC	ATC	ACC	CTA	GAC	AGA	GAT	ACT	CTT	AAA	AGC	CTA	GTG	528
Asn	Pro	Leu	Gly	Ile	Thr	Leu	Asp	Arg	Asp	Thr	Leu	Lys	Ser	Leu	Val	
				165					170					175		
AGC	TTC	ATC	GAT	GAA	AAG	AAC	ATT	CAC	TTT	GTC	TGC	GAT	GAA	ATC	TAT	576
Ser	Phe	Ile	Asp	Glu	Lys	Asn	Ile	His	Phe	Val	Cys	Asp	Glu	Ile	Tyr	
			180					185					190			
GCT	GCC	ACT	CTC	TTC	TGT	CCA	CCC	AAG	TTC	GTA	AGC	GTC	GCT	GAA	GTG	624
Ala	Ala	Thr	Leu	Phe	Cys	Pro	Pro	Lys	Phe	Val	Ser	Val	Ala	Glu	Val	
		195					200					205				
ATC	CAA	GAA	ATG	GAC	TGT	AAT	CTT	GAT	CTC	ATC	CAC	ATT	GTT	TAC	AGT	672
Ile	Gln	Glu	Met	Asp	Cys	Asn	Leu	Asp	Leu	Ile	His	Ile	Val	Tyr	Ser	
	210					215					220					
TTG	TCT	AAG	GAC	ATG	GGC	CTC	CCT	GGC	TTT	AGG	GTT	GGC	ATT	GTT	TAT	720
Leu	Ser	Lys	Asp	Met	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	Tyr	
225					230					235					240	
TCT	TAT	AAT	GAT	GCA	GTT	GTG	AGT	TGT	ATC	CGC	AAG	ATG	TCA	AGC	TTC	768
Ser	Tyr	Asn	Asp	Ala	Val	Val	Ser	Cys	Ile	Arg	Lys	Met	Ser	Ser	Phe	
				245				250					255			
GGT	TTG	GTA	TCC	TCA	CAA	ACT	CAA	TAT	TTA	CTC	GCT	TCA	ATG	CTT	TCT	816
Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Leu	Leu	Ala	Ser	Met	Leu	Ser	
			260					265					270			
GAT	GAT	GAA	TTT	GTG	GAA	AAG	TTT	CTA	GCG	GAA	AGC	TCA	AAG	AGG	CTG	864
Asp	Asp	Glu	Phe	Val	Glu	Lys	Phe	Leu	Ala	Glu	Ser	Ser	Lys	Arg	Leu	
		275					280					285				
GCA	AAA	AGG	TAC	CAT	ATT	TTC	ACA	AAG	AGA	CTT	GAG	AAA	GTG	GGG	ATT	912
Ala	Lys	Arg	Tyr	His	Ile	Phe	Thr	Lys	Arg	Leu	Glu	Lys	Val	Gly	Ile	
	290					295					300					
AAC	TGC	TTG	AAG	GGA	AAT	GCA	GGT	CTT	TTC	TTC	TGG	ATG	GAT	TTG	CGA	960
Asn	Cys	Leu	Lys	Gly	Asn	Ala	Gly	Leu	Phe	Phe	Trp	Met	Asp	Leu	Arg	
305					310					315				320		
CAC	CTC	CTT	CAA	CAA	GAA	ACA	GTT	GAT	GCC	GAA	ATG	AAG	CTA	TGG	GGC	1008
His	Leu	Leu	Gln	Gln	Glu	Thr	Val	Asp	Ala	Glu	Met	Lys	Leu	Trp	Gly	
				325				330						335		

ACG ATT TTG AAC GAT GTG AAA CTT AAC GTT TCA CCA GGC TCT TCC TTT 1056
 Thr Ile Leu Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser Phe
 340 345 350

CAT TGC CAG GAG CCT GGT TGG TTC AGA GTC TGC TTC GCT G 1096
 His Cys Gln Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Asp
 1 5 10 15
 Trp Ile Arg Lys Asn Pro Tyr Ala Ser Ile Cys Thr Ala Glu Gly Val
 20 25 30
 Asp Glu Phe Lys Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro
 35 40 45
 Glu Phe Arg Lys Ala Val Ala Lys Phe Met Gly Lys Val Arg Gly Gly
 50 55 60
 Arg Val Thr Phe Asp Pro Asp Arg Ile Val Met Gly Gly Gly Val Thr
 65 70 75 80
 Gly Ala Asn Glu Gln Ile Ile Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95
 Phe Leu Val Pro Ser Pro Tyr Tyr Pro Ala Phe Asp Arg Asp Leu Gly
 100 105 110
 Trp Arg Thr Gly Gly Glu Ile Val Pro Val Pro Cys Asp Ser Ser Thr
 115 120 125
 Asn Phe Gln Ile Thr Arg Asp Ala Leu Glu Glu Ala Tyr Glu Lys Ala
 130 135 140
 Arg Glu Ala Asn Ile Asn Ile Lys Gly Leu Ile Ile Thr Asn Pro Ser
 145 150 155 160
 Asn Pro Leu Gly Ile Thr Leu Asp Arg Asp Thr Leu Lys Ser Leu Val
 165 170 175
 Ser Phe Ile Asp Glu Lys Asn Ile His Phe Val Cys Asp Glu Ile Tyr
 180 185 190
 Ala Ala Thr Leu Phe Cys Pro Pro Lys Phe Val Ser Val Ala Glu Val
 195 200 205
 Ile Gln Glu Met Asp Cys Asn Leu Asp Leu Ile His Ile Val Tyr Ser
 210 215 220

Leu Ser Lys Asp Met Gly Leu Pro Gly Phe Arg Val Gly Ile Val Tyr
 225 230 235 240
 Ser Tyr Asn Asp Ala Val Val Ser Cys Ile Arg Lys Met Ser Ser Phe
 245 250 255
 Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Ser
 260 265 270
 Asp Asp Glu Phe Val Glu Lys Phe Leu Ala Glu Ser Ser Lys Arg Leu
 275 280 285
 Ala Lys Arg Tyr His Ile Phe Thr Lys Arg Leu Glu Lys Val Gly Ile
 290 295 300
 Asn Cys Leu Lys Gly Asn Ala Gly Leu Phe Phe Trp Met Asp Leu Arg
 305 310 315 320
 His Leu Leu Gln Gln Glu Thr Val Asp Ala Glu Met Lys Leu Trp Gly
 325 330 335
 Thr Ile Leu Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser Phe
 340 345 350
 His Cys Gln Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAG ATG GGA TTT GGG GAA AAT CTG CTT TGC TTT GAT TTA GTT CAA GAA	48
Gln Met Gly Phe Gly Glu Asn Leu Leu Cys Phe Asp Leu Val Gln Glu	
1 5 10 15	
TGG GTC TTA AGC AAC CCA GAA GCC TCT ATC TGC ACT GCC GAA GGT ATA	96
Trp Val Leu Ser Asn Pro Glu Ala Ser Ile Cys Thr Ala Glu Gly Ile	
20 25 30	
AGT GAT TTC AGA GAT ATC GCT ATC TTT CAG GAT TAT CAC GGC TTG CCA	144
Ser Asp Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
GAG TTC AGA AAT GCT GTT GCA AAT TTT ATG GCA AGA GTG AGA GGG AAT	192
Glu Phe Arg Asn Ala Val Ala Asn Phe Met Ala Arg Val Arg Gly Asn	
50 55 60	

AGA	GTC	AAA	TAC	GAC	CCT	GAT	CGA	ATT	GTT	ATG	AGC	GGT	GGA	GCA	ACC	240
Arg	Val	Lys	Tyr	Asp	Pro	Asp	Arg	Ile	Val	Met	Ser	Gly	Gly	Ala	Thr	
65					70				75						80	
GGA	GCA	CAT	GAG	ACG	GTT	GCC	TTT	TGT	TTG	GCT	GAT	CCC	GGT	GAA	GCA	288
Gly	Ala	His	Glu	Thr	Val	Ala	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Glu	Ala	
			85					90						95		
TTT	TTG	GGT	GCC	ACT	CCT	TAC	TAT	CCA	GGA	TTT	GGT	CGA	GAT	TTG	AGA	336
Phe	Leu	Gly	Ala	Thr	Pro	Tyr	Tyr	Pro	Gly	Phe	Gly	Arg	Asp	Leu	Arg	
			100					105					110			
TGG	AGA	ACA	GGA	GTT	CAA	CTT	TTT	CCA	GTT	GTG	TGT	GAC	AGT	TCT	AAC	384
Trp	Arg	Thr	Gly	Val	Gln	Leu	Phe	Pro	Val	Val	Cys	Asp	Ser	Ser	Asn	
		115				120						125				
AAT	TTC	AAG	ATT	ACA	AGA	GAA	GCC	GTG	GAA	GCA	GCA	TAT	GAA	AAA	GCT	432
Asn	Phe	Lys	Ile	Thr	Arg	Glu	Ala	Val	Glu	Ala	Ala	Tyr	Glu	Lys	Ala	
	130					135					140					
CAA	GAA	GAC	CAC	ATC	AGA	ATC	AAG	GGT	TTG	GTC	CTC	ACA	AAT	CCA	TCG	480
Gln	Glu	Asp	His	Ile	Arg	Ile	Lys	Gly	Leu	Val	Leu	Thr	Asn	Pro	Ser	
145				150					155						160	
AAC	CCG	CTG	GGG	ACT	TGT	TTG	GAC	AGA	GAA	ACA	CTA	AGA	AGT	TTA	GTA	528
Asn	Pro	Leu	Gly	Thr	Cys	Leu	Asp	Arg	Glu	Thr	Leu	Arg	Ser	Leu	Val	
			165					170						175		
AGC	TTC	ATT	AAT	GAA	AAG	AAC	ATC	CAC	TTA	GTC	TGC	GAC	GAG	ATT	TAT	576
Ser	Phe	Ile	Asn	Glu	Lys	Asn	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	
		180						185					190			
GCT	GCC	ACA	ATC	TTC	ATG	GGC	CAG	CCC	GAT	TTC	ATT	AGC	ATC	TCT	GAA	624
Ala	Ala	Thr	Ile	Phe	Met	Gly	Gln	Pro	Asp	Phe	Ile	Ser	Ile	Ser	Glu	
		195				200						205				
ATT	ATA	GAA	GAA	GAT	ATT	CAC	TGC	AAT	CGC	AAT	CTC	ATC	CAC	CTT	GTT	672
Ile	Ile	Glu	Glu	Asp	Ile	His	Cys	Asn	Arg	Asn	Leu	Ile	His	Leu	Val	
	210					215					220					
TAC	AGT	CTT	TCA	AAG	GAT	CTG	GGG	TTC	CCA	GGC	TTT	AGG	GTC	GGC	ATT	720
Tyr	Ser	Leu	Ser	Lys	Asp	Leu	Gly	Phe	Pro	Gly	Phe	Arg	Val	Gly	Ile	
225				230				235						240		
ATA	TAC	TCA	TAC	AAC	GAT	ACA	GTT	GTG	AGT	TGC	GCC	TGC	AAA	ATG	TCA	768
Ile	Tyr	Ser	Tyr	Asn	Asp	Thr	Val	Val	Ser	Cys	Ala	Cys	Lys	Met	Ser	
				245					250					255		
AGC	TTT	GGA	CTT	GTA	TCA	TCA	CAA	ACT	CAA	CAT	TTA	ATC	GCT	TCA	ATG	816
Ser	Phe	Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	His	Leu	Ile	Ala	Ser	Met	
			260					265					270			
TTA	TCA	GAT	GAT	GAA	TTT	GTG	GAT	AGG	TTC	ATT	ACT	GAG	AGT	GCT	AAA	864
Leu	Ser	Asp	Asp	Glu	Phe	Val	Asp	Arg	Phe	Ile	Thr	Glu	Ser	Ala	Lys	
		275					280					285				
AGG	CTT	GCA	AAA	AGG	CAC	AGA	GCC	TTC	ACA	TGG	GGG	CTA	TCT	CAA	GTA	912
Arg	Leu	Ala	Lys	Arg	His	Arg	Ala	Phe	Thr	Trp	Gly	Leu	Ser	Gln	Val	
	290					295					300					

GGC ATT GGT TGT TTG AAG AGC AAT GCG GGG CTA TTT TTC TGG ATG GAT	960
Gly Ile Gly Cys Leu Lys Ser Asn Ala Gly Leu Phe Phe Trp Met Asp	
305 310 315 320	
TTG CAT CAT CTC CTC AAG GAG CAA ACT GAT GAA GCA GAG ATA GAA CTG	1008
Leu His His Leu Ile Lys Glu Gln Thr Asp Glu Ala Glu Ile Glu Leu	
325 330 335	
TGG AAA GTG ATA ATC AAC GAA GTT AAA TTA AAT GTT TCT CCG GGT TCT	1056
Trp Lys Val Ile Ile Asn Glu Val Lys Leu Asn Val Ser Pro Gly Ser	
340 345 350	
TCC TTT CAT TGC GCT AAT CCA GGA TGG TTT CGG GTT TGT TTC GCC AAC	1104
Ser Phe His Cys Ala Asn Pro Gly Trp Phe Arg Val Cys Phe Ala Asn	
355 360 365	
ATG GAC GAA	1113
Met Asp Glu	
370	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Met Gly Phe Gly Glu Asn Leu Leu Cys Phe Asp Leu Val Gln Glu	
1 5 10 15	
Trp Val Leu Ser Asn Pro Glu Ala Ser Ile Cys Thr Ala Glu Gly Ile	
20 25 30	
Ser Asp Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
Glu Phe Arg Asn Ala Val Ala Asn Phe Met Ala Arg Val Arg Gly Asn	
50 55 60	
Arg Val Lys Tyr Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr	
65 70 75 80	
Gly Ala His Glu Thr Val Ala Phe Cys Leu Ala Asp Pro Gly Glu Ala	
85 90 95	
Phe Leu Gly Ala Thr Pro Tyr Tyr Pro Gly Phe Gly Arg Asp Leu Arg	
100 105 110	
Trp Arg Thr Gly Val Gln Leu Phe Pro Val Val Cys Asp Ser Ser Asn	
115 120 125	
Asn Phe Lys Ile Thr Arg Glu Ala Val Glu Ala Ala Tyr Glu Lys Ala	
130 135 140	
Gln Glu Asp His Ile Arg Ile Lys Gly Leu Val Leu Thr Asn Pro Ser	
145 150 155 160	

Asn	Pro	Leu	Gly	Thr	Cys	Leu	Asp	Arg	Glu	Thr	Leu	Arg	Ser	Leu	Val	165	170	175
Ser	Phe	Ile	Asn	Glu	Lys	Asn	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	180	185	190
Ala	Ala	Thr	Ile	Phe	Met	Gly	Gln	Pro	Asp	Phe	Ile	Ser	Ile	Ser	Glu	195	200	205
Ile	Ile	Glu	Glu	Asp	Ile	His	Cys	Asn	Arg	Asn	Leu	Ile	His	Leu	Val	210	215	220
Tyr	Ser	Leu	Ser	Lys	Asp	Leu	Gly	Phe	Pro	Gly	Phe	Arg	Val	Gly	Ile	225	230	235
Ile	Tyr	Ser	Tyr	Asn	Asp	Thr	Val	Val	Ser	Cys	Ala	Cys	Lys	Met	Ser	245	250	255
Ser	Phe	Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	His	Leu	Ile	Ala	Ser	Met	260	265	270
Leu	Ser	Asp	Asp	Glu	Phe	Val	Asp	Arg	Phe	Ile	Thr	Glu	Ser	Ala	Lys	275	280	285
Arg	Leu	Ala	Lys	Arg	His	Arg	Ala	Phe	Thr	Trp	Gly	Leu	Ser	Gln	Val	290	295	300
Gly	Ile	Gly	Cys	Leu	Lys	Ser	Asn	Ala	Gly	Leu	Phe	Phe	Trp	Met	Asp	305	310	315
Leu	His	His	Leu	Leu	Lys	Glu	Gln	Thr	Asp	Glu	Ala	Glu	Ile	Glu	Leu	325	330	335
Trp	Lys	Val	Ile	Ile	Asn	Glu	Val	Lys	Leu	Asn	Val	Ser	Pro	Gly	Ser	340	345	350
Ser	Phe	His	Cys	Ala	Asn	Pro	Gly	Trp	Phe	Arg	Val	Cys	Phe	Ala	Asn	355	360	365
Met	Asp	Glu														370		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAYTTYGAYG GNTGGAARGC

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCRTCCATRT TNGCRAARCA

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CARATGGGNY TNGCNGARAA

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCRAARCANA CNCKRAACCA

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTGATCARA TGGGNYTNGC NGARAA

26

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCTGCAGCR AARCANACNC KRAACCA

27